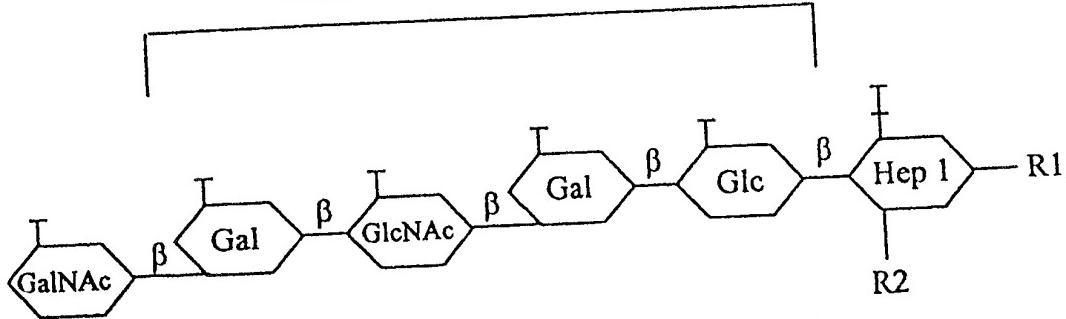


U.S. PRO
JC958 10/007267
12/03/01

Lacto-N-neotetraose



1-1-M

3F11 & 9-2-L387

2-1-L8 & 4C4

Monoclonal Antibodies

17-1-L1

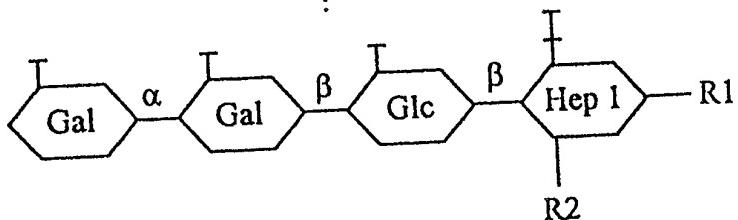


FIG. 1

LOS Locus

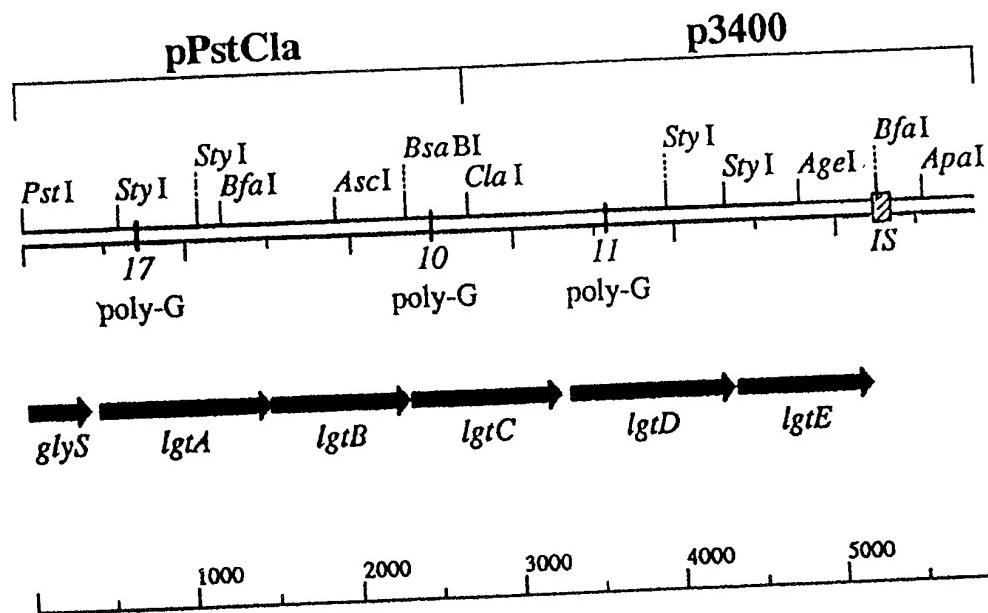


FIG. 2A

FIG.2B-1

SOURCE *Neisseria gonorrhoeae*.
 ORGANISM *Neisseria gonorrhoeae*
 source 1..5859

```

CDS <1..381
      /gene="glyS"
      /codon_start=1
      /transl_table=11
      /product="glycyl tRNA synthetase beta chain"

/translation="LQAVAVFKQLPEAAALAANRKVQNLKADAALGEVNESLLQQ
DEEKALYAMAQGLQPKIAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDAAVKQ
NRLLNRLAEQMNAVADIALLGEE"

CDS 445..1491
      /gene="lgtA"
      /codon_start=1
      /function="adds GlCNAC to lacto-N-neotetraose chain of
gonococcal LOS"
      /evidence=experimental
      /transl_except=(pos:445..447,aa:Met)
      /transl_table=11
      /product="glycosyl transferase"

/translation="MQPLIVSVLICAYNVEKYFAQSLSAAVNNQTWRNLIDILIVDDGSTD
GTIAIAKDFQRKDSRIKILQAQNSGLIPSINIGLDELAKSGGGGEYIARTDADDIA
SPGWIEKIVGEMEIKDRSIIAMGAWILEVSEKDGNRLLAREHHKGKIWWKKPTRHEDIAA
FFPFGNPPIHNNTMIRRSVIDGGLRYDTERDWAEDYYQFWYDVSKLGRLLAYYPEALVKY
RHHANQVSSKHSVRQHETAQGIQKTAARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEK
DLPEEDFERARFLYQCFKRTDTPPSGAWLDFAADGRMRRLFITLQRQFGILYRLIKNR
RQARSDSAGKEQEI"
  
```

FIG. 2B-2

```

CDS
/gene="lgtB"
/codon_start=1
/function="adds second galactose to the lacto-N-tetraose
chain in LOS"
/evidence=experimental
/product="glycosyl transferase"

/translation="MQNHVISLASAAERRAIIAATFGSRGIPFQFFDALLMPSERLERA
MAELVPGLSAHPYILSGVTEKACFMSHAVLWEQALDEGVPPYIAVEFDVVLLGEQAEQFLA
EDTWLQERFDPDPSAFVRLETMFMHVTLSPTSGVADYGGRAFFPILESEHCGTAGYIISR
KAMRFFLDRAVLPPERLHPVVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQN
SALGSLLIEHRRLINKQQWRDSPANTFKHRLIRALTIGREREKRRQRREQLIGKIV
PFQ"

```

2342..3262

```

CDS
/gene="lgtC"
/codon_start=1
/function="adds galactose alpha(1-4) to Gal-Glc in
gonococcal LOS"
/evidence=experimental
/transl_table=11
/product="glycosyl transferase"

/translation="MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAAGISEEEN
RAAVAANLRGGGNIRFIDVNIPEDFAGFPLNIRHISITTYARLKLGEYIADCDCDKVLYLD
TDVLVRDGILKPLWDTDLGGNNWVGACIDLFEVERQEGYKQKIGMADGEYYFNAGVLLINL
KKWRRHDIFKMSCEWVEQYKDVDMQYQDQDILINGLFKGGVVCYANSRRFNMPTNYAFMAN
GFASRHTDPLYLDRNTAMPVAVSHYCGSAKPKWHRDCTVNGAERTFTELAGSLTIVPEE
WRGKLVAVPTKCMIQWRWKLSARFLRKIY"

```

FIG.2B-3

```

CDS          3322..4335
            /gene="1gtD"
            /codon_start=1
            /function="adds terminal GalNAc to lacto-N-neotetraose
            chain of LOS"
            /evidence=experimental
            /transl_except=(pos:3322..3324,aa:Met)
            /transl_table=11
            /product="glycosyl transferase"

            /translation="MQPLVSVLICAYNAEKYFAQSLAAAVVGQTWRNLDILIVDDGSTD
GTPAIARHFFQEQQDGRIRIISNPNRLGFIASLNIGDELAKSGGGEYTARTDADDIASP
GWIEKRVGEMEKDRSIIAMGAWLEVLSEENNKSVLAAITARGAIWDKRPTRHEDIVAVF
FFGNPIHNNTMIMRRSVIDGGLRFDPAYTHAEDYKFWYEAGKLGRLLAYPEALVKYRF
HQDQTSSKYNLQQRRTAWKIREEIRAGYWKAGGIAVGADCLNYGLRKSTAYALYEKAL
SGQDIGCLRLFLYEXFLSLEYKSLTDLDFLTDRVMRKLFAAPQRKILKKMLRPWKY
RSY"          CDS          4354..5196
            /gene="1gtE"
            /codon_start=1
            /function="adds first galactose to lacto-N-neotetraose
            chain of LOS"
            /evidence=experimental
            /transl_table=11
            /product="glycosyl transferase"

            /translation="MONHVTSLASAERRAHIAADTFGSRGIPFQFFDALMPSERLEQA
MAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVETEDDVLLGEGAEQFLA
EDTWLEERFDKDSSAFIVRLETMFAKVTVRPDFKVNENRSFPLLESEHCCTAGYIISR
EAMRFFLDRAFLPPERIKAVDLMMEFYFFDEKEGMPVYQVSPALCTQELHYAKFLSQN
SMLGSDELDREQGRRHRRSLLKVMFDLKRALGKFGREKKRMRQAELEKRVYGRVV
TLFR"

```

FIG.2B-4

BASE COUNT	1412 a	1462 c	1661 g	1324 t
ORIGIN				
1	ctggcaggcc	tgcggcgatt	caaaaactg	ccgaaaggcc
61	aaacgcgtgc	aaaacctgct	aaaaaaagcc	atggcgaaat
121	ctgctgcaac	aggacgaaaga	aaaaggccctg	gcggccgaaa
181	attggccggcg	ccgtcgccga	cgaaccgttcc	cgcaagggtt
241	aagccgcagg	ttgatggcctt	cttcgacggc	tgctccgaaact
301	aaacaaaaac	gcctgtgaaacct	gtgtgggtga	tgccggccgta
361	atcgcgcttt	tggcgagta	accgttgtac	gtgtggccgac
421	gcataaattt	atcgggagag	taaatttgcag	tgaaatcagac
481	aacgtaaaaa	aatattttgc	ccaatcatta	gtggcagggc
541	ttggatattt	tgattgtcga	tgacgggctcg	agatggccat
601	tttcaaaaaggc	gggacagggcg	tgatcaaattc	cttgcacaag
661	ccctctttaa	acatcgggct	ggacgaaattg	ctaaaaatttc
721	attggcgcca	ccgatggccga	cgatattgcc	ccccccgtt
781	gagatggaaa	aagacccgcag	catcatgcg	gggggggggg
841	gaaaaggacg	gcaaccggct	ggcgcgccac	gggggggggg
901	acccggcacg	aagacatcgcc	cgcccttttc	gggggggggg
961	atgattatgc	ggcgccagcgt	cattgacggc	gggggggggg
1021	gcggaaaggatt	accaatttttgc	gtacgatgtc	tttttttttt
1081	gaaggcttgg	tcaaataccg	catttcacggc	tttttttttt
1141	caacacgaaa	tgcggcaagg	cattccaaaaaa	tttttttttt
1201	ggttttaaaa	cccggttcga	cacccttagaa	tttttttttt
1261	ctggccggaga	aggatttgcc	ggaaagaagat	tttttttttt
1321	tgcttcaaac	ggacggacac	ggcgccctcc	tttttttttt
1381	aggatggggc	ggctgtttac	tttgaggccaa	tttttttttt
1441	aaccggccggc	aggcgcggtc	ggatttggccaa	tttttttttt
1501	acgttatcag	tttggcttcc	gcaaaaaaaa	tttttttttt
1561	gtcggggcat	cccggtccag	gtctgaaagg	tttttttttt

FIG.2B-5

1621	caatgggaaa	actcgcccc	ggcttgtcgg	cgcaccccta	tttgagggaa	gtggaaaaaaag
1681	cctgcttat	gagccacgcc	gtatgtggg	aacaggcatt	ggacgaaggc	gtaccgtata
1741	tcggcgat	tgaagatgt	gtcttactcg	gcgaaggcgc	ggaggagttc	cttgcgcgaaag
1801	atacttggct	gcaagaacgc	tttgaccccg	attccgcctt	tgtcgcccg	ttggaaaacgaa
1861	tgttatgca	cgtcctgacc	tcgcccctcg	gctacggggaa	cgcgccttcc	cgcgggggg
1921	cgctttgga	aagcgaacac	tgcgggacgg	cgggctatat	tattccgaa	aaggcgatgc
1981	gtttttctt	ggacagggtt	gccgttttgc	cgtccgaacg	cctgaccctt	gtcgattttga
2041	tgatgttcgg	caaccctgac	gacagggaaag	gaatgccggt	ttgcagctc	aatccccggct
2101	tgtgcggcc	agagctgcat	tatgccaagt	ttcacgacca	aaacagcgc	ttggcagcc
2161	tgatcgaaaca	tgacccggcc	ctgacccgca	aacgcaatg	gcccggattcc	ccggccaaaca
2221	cattcaaaca	ccgcctgtatc	cgcgccttga	ccaaaatcg	caggaaagg	gaaaaacgccc
2281	ggccaaaggcg	cgaacagttt	atcgccaaaga	ttatgtgcc	tttccaataa	aaggagaaaa
2341	gatggacatc	gtattttcg	cagacgacaa	ctatggccgc	taccttgcg	ttggggccaa
2401	aagcggtggaa	gcggcccatc	ccgatacgg	aatcagggttc	cacgtcctcg	atgcggccat
2461	cagtggggaa	aaccgggggg	cggttggccgc	caatttgcgg	gggggggtta	atatccgctt
2521	tatagacgtt	aaccccgaaag	atttcggccgg	cttcccccata	aacatcaggc	acattttccat
2581	tacgacttat	gccccggcctga	aattttggcga	atacatttgc	gatttgcaca	aagtctgtt
2641	tctggatatacg	gacgttatgg	tcagggacgg	ccttgcggcc	ttatggata	ccgattttggg
2701	cggtaactgg	gtcggcgctgt	gcatcgattt	gtttgtcgaa	aggcaggaaag	gatacaaaca
2761	aaaaaatcggt	atgggggacg	gagaataatta	tttcaatgc	ggcgtatttgc	tgatcaacactt
2821	gaaaaaagtgg	cgggggcact	atattttca	aatgtcctgc	gaatgggtgg	aacaataaca
2881	ggacgtgtatg	caatatacg	atcaggacat	tttgaacgg	ctgttttaag	gcgggggtgt
2941	ttatgcgaac	agccgtttca	actttatgc	gaccaattat	gcctttatgg	cgaaacgggtt
3001	tgcgtccgc	cataccgacc	cgctttacat	cgaccgttac	aatacggcga	tgcccggtcgc
3061	cgtcagccat	tatgcggct	cgccaaaggc	gtggccacagg	gactgcacgg	tttgggggtgc
3121	ggaacgtttc	acagagtgg	ccggcaggct	gacgaccgtt	cccgaaagaat	ggcgccggca
3181	acttgcgtc	ccggccgacaa	ccggcaggctt	tcaaaatgtgg	cgcaaaaaaggc	tgtctggccag
3241	attcttagc	aagattttatt	gacggggggcag	ccgcgtctgaa	ggcatcgac	ggcattacaaac
3301	gtatcgaaa	ggagaaaaacgg	attgcagccat	tattgtcagcg	tattgtatttgc	cgccctacaaac
3361	gcagaaaaat	atttggccc	atcatatttggcc	ggcgtagtgg	ggcagacttgc	gtgggggggg

FIG. 2B-6

3421 gatattttga ttgtcgatga cggctcgacgg gacggcacgc cggccatttc
 3481 caagaacagg acggcaggat cagggataatt tccaatcccc gcaattttggg ctttatcgcc
 3541 tctttaaaca tcgggcttggca cgaatttgaa cttcccccggc aagtccccggg tattggcgcc
 3601 accgatgccc accgatattgc acgttgc gatggggcg gatggatggaa aaatcggtgg
 3661 aaagaccggca gcatcattgc tgcccgccat ttgttggaa gggatggaa agaaaacaat
 3721 aaaaggcgttc ttggccgttc tgcccgaaac ggcccaattt gggacaacc gaccggccat
 3781 gaagacattt cgcccggttt ccctttcgcc aaccaccatac acaacaacac gatgattatq
 3841 aggccaggcg tcattgacgg cgggttgcgg ttcgatccag cctatatcca cgccgaagac
 3901 tataaaggttt ggtacgaagg cggccaaactg ggcaggctgg cttattatcc cgaaggccttq
 3961 gtcaaaatacc gcttccatca agaccagact tcttccaaat acaacacctgca acagcgcagg
 4021 acggcgttggaa aatatcaaaga agaaatcagg gcccgggtttt ggaaggccggc aggcatagcc
 4081 gtcggggggg actggcctgaa ttacgggctt ttgaaaatcaa cggcatatgc gttgtacgaa
 4141 aaaggcccttgc cgggacaggaa tatcggtatgc ctccggcctgt tcctgtacg atatttcttq
 4201 tcgttggaaa agtattttt gaccgatttt ctggattttc tgacagacccg cgtgatgggg
 4261 aagctgttttgc cggcacccgaa atataggaaaa atcctgaaaa aaatgttacg cccttggaaa
 4321 tacggcaggat attggaaaccc aacaggataa atcatgcaa accacgttat cagttggct
 4381 tccggcccgag agccggggc gcacatttgcg gataccttgcg gtagtcgcg catcccggtt
 4441 cagttttgc acgactgt gccgtctgaa aggctggaaac aggctggaa aaccgttgcg ggaactcgtc
 4501 cccggcttgt cggggcaccc ctatttgcg ggagggtggaaa aagccgttgc aagccgtt
 4561 gccgttattgt gggAACAGGC gttggatgaa ggtctggccgt atatcgccgt atttgggg
 4621 gacgttttac tcggcgaagg cggggaggcgttggccg aagataacttg gttggaaagg
 4681 cgttttgcaca agggatccgc ttatcgatgc ttcccttgcg aacccgttgc gaaagtatt
 4741 gtcaagccgg ataaaagtcc gaattatgaa aaccgggtcat ttcccttgcg aacccgttgc
 4801 cattgtggaa cggctggcta tattatcc cgttggccgaa tgatgtatgt tacttatttc
 4861 ttggccgtt tgccggccaga gcggattaaa gcggatgaa cttatgtac ccaagaattt
 4921 ttgtataagg agggatgcc ttgtttatcag gtttagtcccg cttatgtac ccaagaattt
 4981 catatgcca agtttctcag tcaaaaacagt atgtttggta gcgatgttggaaa
 5041 gaacaaggaa gaagacaccg ccgttcgtt aagggtatgt ttgacttgcgatgt
 5101 ggttaatttcg gtagggaaaa atggaggcgtt aatggaggcgtt
 5161 aaagtttacg gcaggcggtt catattgttc aaatagtttgcgatgttggatata
 agggattaa

FIG.2B-7

5221	aatcagaaaat	ggacacactg	tcattcccg	gcagggcg	ttaaacttcg
5281	gtttttccg	ataaattctt	gccgcattaa	aattccagat	atcttaggtct
5341	cggcggggg	atttgtctt	tttcggataa	aatcccgtgt	tcccgctttc
5401	atcgccccaa	agcgctctgca	tcgcggcgat	ggcggcgagt	gcggggatga
5461	aatccgtttt	ccgagggttaa	ccgcctgtaaa	gggggggttt	ttttcatctt
5521	ttctgtccag	ccgccttcgg	gcccggaccat	ctgtgggtttt	gtttaggtaa
5581	gtcgccgagt	ttgcagggcg	ggttgtatgt	cataatcagg	ctgtgggtttt
5641	tttgtcgagt	gcttcacgg	agccgatgt	tttttttttt	gttttttttt
5701	gctttttcg	cacggggaga	tgacgatttc	gggggggggg	tttttttttt
5761	ttctcgtcg	aggcggacga	tgcagggttc	gggggggggg	tttttttttt
5821	gagttcgacg	cttttttgc	gggttggaaatc	catggatc	tttttttttt

1gtA	1	LQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTTLAIA	50
1gtD	1	LQPLVSVLICAYNAEKYFAQSLAAVGQTWRLNLDILIVDDGSTDGTTPAIA	50
1gtA	51	KDFQKRDSRIKILQAQNSQLIPSLNIGLDELAKSGGGGEYIARTDADD	100
1gtD	51	RHFQEQQDGRIRITISNPRNLGFIASLNIGLDELAKS. .GGGEYIARTDADD	98
1gtA	101	IASP瓜IEKIVGEMEKDRSIIIAMGAWILEVLSEEKDGNRLLARHHKHGKIWK	150
1gtD	99	IASP瓜IEKIVGEMEKDRSIIIAMGAWILEVLSEEENNKSVLAAIARNGAIWD	148
1gtA	151	KPTRHEDIAAFFPFGNPIHNNNTMIMRRSVIDGGLRYDTERDWAEDYQFWY	200
1gtD	149	KPTRHEDIVAVFPFGNPIHNNNTMIMRRSVIDGGLRFDPAYIHAEDYKFWY	198

FIG. 3A

1gtA 201 DVSKLGRLLAYYPEALVKYRLHANQVSSKHSVRQHEIAQQGIQKTARNDFLQ 250
1gtD 199 EAGKLGRLLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKEEIRAGYWIK 248

1gtA 251 SMGFKTRFDSSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP 300
1gtD 249 AAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGHCLRLFLYEYFLSLEKY 298

1gtA 301 PSGAWLDFAADGRMRRLFTRLQYFGILYRLIKNRR 335
1gtD 299 SLTDLDFLTDRVMRKLFAAPQYRKILKKMLRPWIK 333

FIG. 3B

1gtB	1	MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVP	50
1gtE	1	MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVP	50
1gtB	51	GLSAHLYLSGVKEKACFMSSHAVLWEQALDEGLPYIAVFEVVLLGEGAEQF	100
1gtE	51	GLSAHPYLSSGVKEKACFMSSHAVLWEQALDEGLPYIAVFEVVLLGEGAEQF	100
1gtB	101	LAEDTTLQERFDPSAFVVRLETMFMHVLTSPSGVADYGGRAFPPLLESEH	150
1gtE	101	LAEDTTLERFDKDSAFIVRLETMFAKVIVRPDKVLNYYENRSFPLLESEH	150
1gtB	151	CGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQL	200
1gtE	151	CGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFYTFFDKEGMPVYQV	200

FIG. 4A

1gtB 201 NPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQRRDSPANTFKHRLI 250

1gtE 201 SPALC^TQELHYAKFLSQNSMILGSQDLEKD . . . REQGRRHRRSLKVMFDLK 246

1gtB 251 RALT^KI^RGREKRRKRR . . . EQTIGKIIIVPFFQ 279

1gtE 247 RALGKF^GREKKR^MERQRQAEL^EKVYGRRVILFK 280

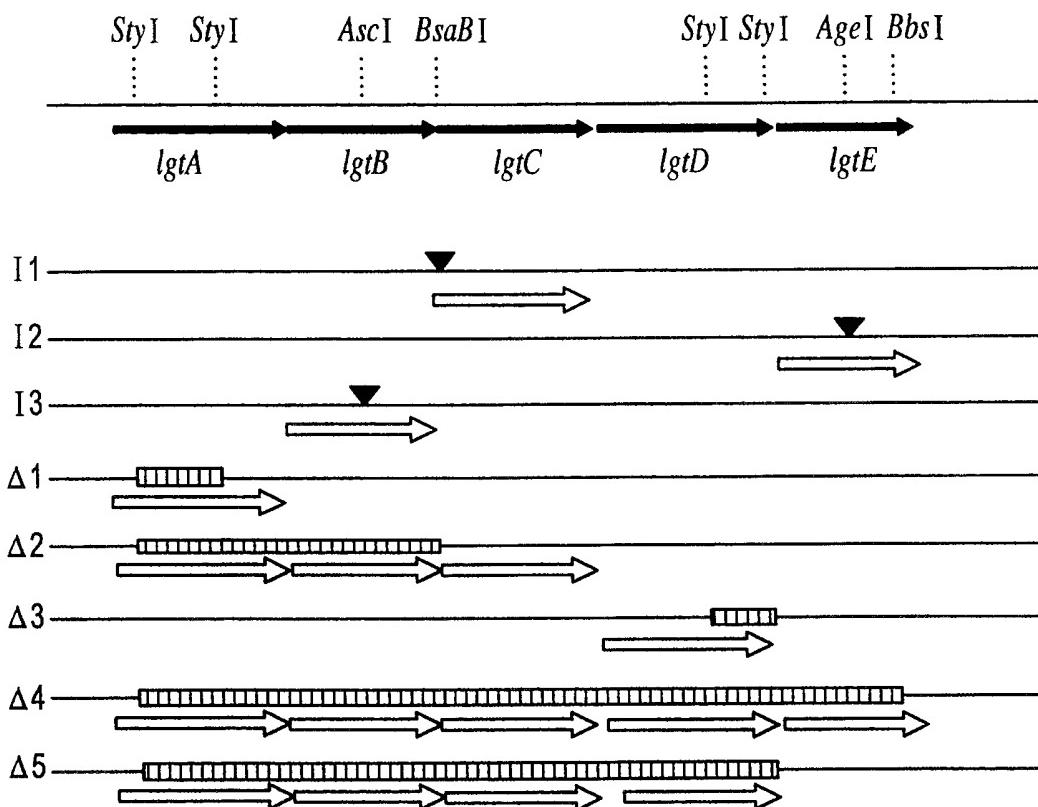
FIG. 4B

FIG. 5A

rfaI	225	NMLLADKLIIFADIKYNTQFSLNYQLKESFINPVTNDTIFI	264
1gtc	192	NGLFKGGVCYANSRFNF.MPTNYAFMANGFASRHTDPLYLDRNTAMPVA	240
rfaI	265	HYIGPTKPKWHDWAWDYPVVSQAFMEAKNASPWKNTALLKPNNSQLRYS	312
1gtc	241	VSHYCGSAKPKWH...RDCTVWGAERFTELAGSL..TVPEEWRGKLAVPP	285
rfaI	313	AKHMLKKHRYLKGFNSNYLFYFI	334
1gtc	286	TKCML..QRWRKKLSARFLRKI	305

FIG. 5B

FIG.6



7188-039

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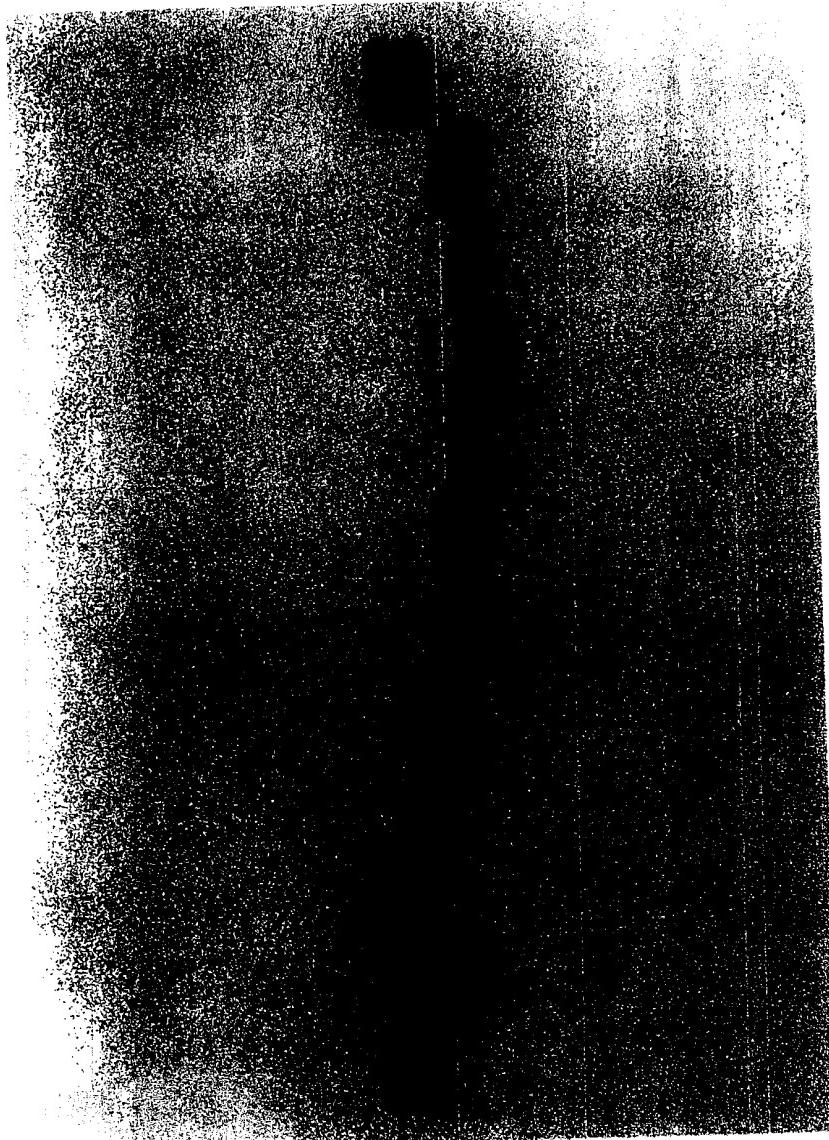


FIG. 7

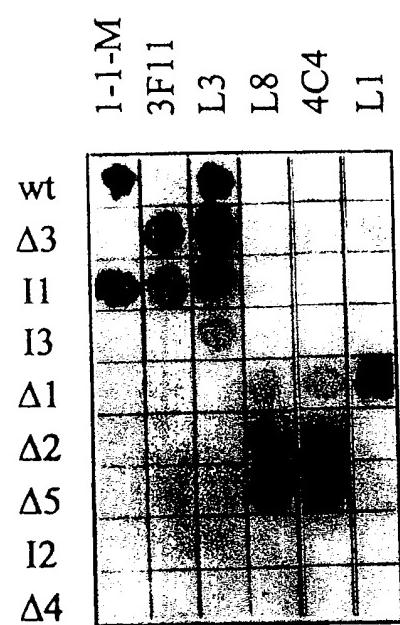


FIG.8